

Inventor: Shankar Subramaniam
Serial No.: 09/882,359
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experimentation. The invention is directed to a method of identifying sequence boundaries in genomic DNA. The method can be used to determine which regions of genomic DNA are included in an expressed polynucleotide. The method includes, in pertinent part, contacting a population of addressed fragments of eukaryotic genomic DNA with a target polynucleotide that binds a terminal sequence of a DNA region and determining a relative order for 2 or more of the addressed fragments compared to a sequence of the genomic DNA. The objected step of determining the relative order of addressed fragments is sufficiently described in the application to enable one skilled in the art to practice the claimed invention. Further, methods for identifying the relative order of addressed fragments are similarly well known to one skilled in the art.

The application teaches on page 7, line 23 through page 8, line 25, that addressed DNA fragments in a population refers to DNA that is bound to a substrate and distinguishable from others in the population according to, for example, a fixed location on a surface by coordinates identifying its location. The application further teaches, for example, on page 11, lines 7-24, that a target polynucleotide complementary to a terminal sequence of region of genomic DNA sequence is bound to sequences flanking a boundary within the genomic DNA. The location at which binding occurs in the genomic DNA is determined in the population of addressed fragments "[b]ecause the fragments are addressed [and] can be ordered with respect to the genomic DNA sequence." Following these teachings, one skilled in the art will understand that the methods of the invention employ a known

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target polynucleotide as a binding probe against a population of genomic DNA fragments indexed in such a way that positive binders can be easily matched by virtue of the genomic DNA address in the population sample.

The application additionally teaches, for example, on page 38, line 31 through page 39, line 18:

The location of the terminal sequence in the genomic DNA fragment can be identified by obtaining a sequence of the fragment and orienting the fragment with respect to other fragments in the population by aligning the sequences of the fragments with the sequence of the genomic DNA. The sequence of a fragment in the addressed population can be obtained using well known methods for nucleotide sequence analysis . . . [or] from prior knowledge of the sequence of the fragment due to indexing of the addressed population. An index of an addressed population includes determination of the sequence for genomic DNA fragments at particular addresses in the population based on sequencing or on a reference sequence used to direct synthesis of the fragment.

Given these teachings and guidance, one skilled in the art will understand that the methods of the invention determine the

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relative order for two or more of the addressed genomic DNA fragments by, for example, merely aligning the sequence of the addressed fragments with the sequence of the genomic DNA. As taught in the application, methods for sequencing DNA are well known in the art and the nucleotide sequence for numerous genomes have been determined (see, for example, page 39, lines 8-11, and page 13, lines 23-32). As such, determining the relative order of addressed fragments is sufficiently enabled and does not require undue experimentation because all that is required, for example, is the alignment of known or determined genomic DNA sequences to obtain the order the corresponding addressed fragments.

Further, the application is replete with descriptions of, for example, methods to obtain genomic DNA, target DNA, address fragments by applying or synthesizing on a substrate and identifying patterns or constellations of target polynucleotides bound to a terminal sequence of a DNA region. Accordingly, the application teaches with sufficient detail for practicing the claimed invention without undue experimentation methods for indexing genomic DNA by addressing it to a substrate, contacting it with a known target polynucleotide, determining the binding of the target polynucleotide and aligning the bound addressed fragments of genomic DNA to its corresponding sequence for identification of a sequence boundary. Such description is sufficient to meet the enablement requirement under 35 U.S.C. §112, first paragraph. Accordingly, Applicant respectfully requests that this ground of rejection be withdrawn.

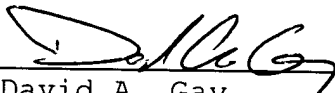
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CONCLUSION

In light of the Amendments and Remarks herein, Applicants submit that the claims are now in condition for allowance and respectfully request a notice to this effect. The Examiner is invited to call the undersigned agent or Cathryn Campbell if there are any questions.

Respectfully submitted,

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Date



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